*The Plant Journal* (1998) **15**(6), 853–857

# Author index


Albrecht, C., Geurts, R., Lapeyrie, F. and Bisseling, T. *Endomycorrhizae and rhizobial Nod factors both require SYM8 to induce the expression of the early nodulin genes* PsENOD5 *and* PsENOD12A 605
Ap Rees, T. *see* Zeeman, S.C.
Atkinson, R.G., Bieleski, L.R.F., Gleave, A.P., Janssen, B.-J. and Morris, B.A.M. *Post-transcriptional silencing of chalcone synthase in petunia using a geminivirus-based episomal vector* 593
Ayaydin, F. *see* Kovács, I.

Babiychuk, E., Cottrill, P.B., Storozhenko, S., Fuangthong, M., Chen, Y., O'Farrell, M.K., Van Montagu, M., Inzé, D. and Kushnir, S. *Higher plants possess two structurally different poly(ADP-ribose) polymerases* 635
Bailey-Serres, J. *see* Fennoy, S.L.
Baker, A. *see* Pool, M.R.
Barker, S.J., Stummer, B., Gao, L., Dispain, I., O'Connor, P.J. and Smith, S.E. *A mutant in* Lycopersicon esculentum *Mill. with highly reduced VA mycorrhizal colonization: isolation and preliminary characterisation* 791
Barratt, D.H.P. *see* Lovegrove, A.
Bartels, D. *see* Frank, W.
Beachy, R.N. *see* Kahn, T.W.
Beachy, R.N. *see* Más, P.
Beale, M.H. *see* Lovegrove, A.
Beale, S.I. *see* Cornejo, J.
Bennett, M.J. *see* Maathius, F.J.M.
Betteridge, A. *see* Boevink, P.
Bharathi, M. *see* Rao, K.V.
Bieleski, L.R.F. *see* Atkinson, R.G.
Bisseling, T. *see* Albrecht, C.
Blackman, L.M., Gunning, B.E.S. and Overall, R.L. *A 45 kDa protein isolated from the nodal walls of* Chara corallina *is localised to plasmodesmata* 401
Boevink, P., Oparka, K., Santa Cruz, S., Martin, B., Betteridge, A. and Hawes, C. *Stacks on tracks: the plant Golgi apparatus traffics on an actin/ER network* 441
Bolwell, G.P. *see* Brown, I.
Borisjuk, L., Walenta, S., Weber, H., Mueller-Klieser, W. and Wobus, U. *A single nuclear locus is involved in both chloroplast RNA* trans*-splicing and 3′ end processing* 583
Borrias, M. *see* Rook, F.
Bosnich, W. *see* Rutledge, R.
Bottka, S. *see* Kovács, I.
Bowen, H.C. *see* Maathius, F.J.M.
Bown, D.P. *see* Rao, K.V.
Braam, J. *see* Campbell, P.
Bray, C.M. *see* West, C.E.
Brennicke, A. *see* Giegé, P.
Brennicke, A. *see* Zabaleta, E.
Bringloe, D. *see* Wan, J.
Brown, I., Trethowan, J., Kerry, M., Mansfield, J. and Bolwell, G.P. *Localization of components of the oxidative cross-linking of glycoproteins and of callose synthesis in papillae formed during the interaction between non-pathogenic strains of* Xanthomonas campestris *and French bean mesophyll cells* 333
Brown, J.W.S. *see* Simpson, C.G.
Brown, S. *see* Hamilton, A.J.
Browse, J. *see* McConn, M.
Byrne, J. *see* Dehesh, K.

Caliskan, M. and Cuming, A.C. *Spatial specificity of $H_2O_2$-generating oxalate oxidase gene expression during wheat embryo germination* 165
Cameron-Mills, V. *see* Rouster, J.
Campbell, P. and Braam, J. *Developmental abnormalities associated with deoxyadenosine methylation in transgenic tobacco* 553
Carninci, P. *see* Seki, M.
Carrera, E. and Prat, S. *Expression of the Arabidopsis* abi1-1 *mutant allele inhibits proteinase inhibitor wound-induction in tomato* 765
Cejudo, F.J. *see* Domínguez, F.
Chan, M.-T. and Yu, S.-M. *The 3′ untranslated region of a rice α-amylase gene mediates sugar-dependent abundance of mRNA* 685
Chattopadhyay, S., Puente, P., Deng, X.-W. and Wei, N. *Combinatorial interaction of light-responsive elements plays a critical role in determining the response characteristics of light-regulated promoters in* Arabidopsis 69
Chaudhury, A. *see* Glover, J.
Chen, Y. *see* Babiychuk, E.
Chengappa, S. *see* Crombie, H.J.
Cheong, Y.H., Yoo, C.M., Park, J.M., Ryu, G.R., Goekjian, V.H., Nagao, R.T., Key, J.L., Cho, M.J. and Hong, J.C. *STF1 is a novel TGACG-binding factor with a zinc-finger motif and a bZIP domain which heterodimerizes with GBF proteins* 199
Chiltz, A. *see* Lebrun-Garcia, A.
Cho, H.-T. and Kende, H. *Tissue localization of expansins in deepwater rice* 805
Cho, M.J. *see* Cheong, Y.H.
Chou, M.-L. and Yang, C.-H. FLD *interacts with genes that affect different developmental phase transitions to regulate* Arabidopsis *shoot development* 231
Chou, W.-M. and Kutchan, T.M. *Enzymatic oxidations in the biosynthesis of complex alkaloids* 289
Chow, K.S., Singh, D.P., Walker, A.R. and Smith, A.G. *Polyunsaturated membranes are required for photosynthetic competence in a mutant of* Arabidopsis 531
Christou, P. *see* Rao, K.V.
Chueca, A. *see* Jaramillo, J.L.
Conner, T. *see* Ruan, Y.
Cooper, B. *see* Kahn, T.W.
Cornejo, J., Willows, R.D. and Beale, S.I. *Phytobilin biosynthesis: cloning and expression of a gene encoding soluble ferredoxin-dependent heme oxygenase from* Synechoscystis *sp. PCC 6803* 99
Corrado, G. *see* Van Blokland, R.
Côté, C. *see* Rutledge, R.
Cottrill, P.B. *see* Babiychuk, E.
Craig, S. *see* Glover, J.
Crombie, H.J., Chengappa, S., Hellyer, A. and Reid, J.S.G. *A xyloglucan oligosaccharide-active, transglycosylating β-D-glucosidase from the cotyledons of nasturtium (*Tropaeolum majus *L) seedlings – purification, properties and characterization of a cDNA clone* 27
Crosby, W.L. *see* Wang, H.
Cuming, A.C. *see* Caliskan, M.
Cutler, A.J. *see* Wang, H.


© 1998 Blackwell Science Ltd

Day, A. *see* Zubko, M.K.
Dehesh, K., Edwards, P., Fillatti, J., Slabaugh, M. and Byrne, J. *KAS IV: a 3-ketoacyl-ACP synthase from* Cuphea *sp. is a medium chain specific condensing enzyme* 383
Deng, X.-W. *see* Chattopadhyay, S.
Dennis, E. *see* Glover, J.
Di Sansebastiano, G.-P., Paris, N., Marc-Martin, S. and Neuhaus, J.-M. *Specific accumulation of GFP in a non-acidic vacuolar compartment via a C-terminal propeptide-mediated sorting pathway* 449
Dietrich, P. and Hedrich, R. *Expression of snowdrop lectin (GNA) in transgenic rice plants confers reistance to rice brown planthopper* 479
Dispain, I. *see* Barker, S.J.
Doering-Saad, C. *see* Perfect, S.E.
Domínguez, F. and Cejudo, F.J. *A gene encoding phosphatidylinositol-4-phosphate 5-kinase is induced by water stress and abscisic acid in* Arabidopsis thaliana 569
Driscoll, B.T. *see* Miller, S.S.
Dudits, D. *see* Kovács, I.
Durner, J. *see* Guo, A.

Edwards, P. *see* Dehesh, K.
Engström, P. *see* Tandre, K.

Faure, J.-D., Gingerich, D. and Howell, S.H. *An Arabidopsis immunophilin, AtFKBP12, binds to AtFIP37 (FKBP interacting protein) in an interaction that is disrupted by FK506* 783
Fennoy, S.L., Nong, T. and Bailey-Serres, J. *Transcriptional and post-transcriptional processes regulate gene expression in oxygen-deprived roots of maize* 727
Fillatti, J. *see* Dehesh, K.
Fischer, K. and Schopfer, P. *Physical strain-mediated microtubule reorientation in the epidermis of gravitropically or phototropically stimulated maize coleoptiles* 119
Fobert, P. *see* Rutledge, R.
Fowke, L.C. *see* Wang, H.
Frank, W., Phillips, J., Salamini, F. and Bartels, D. *Two dehydration-inducible transcripts from the resurrection plant* Craterostigma plantagineum *encode interacting homeodomain-leucine zipper proteins* 413
Fu, X. *see* Rao, K.V.
Fuangthong, M. *see* Babiychuk, E.
Furuya, M. *see* Kim, B.C.
Furuya, M. *see* Uchida, K.

Gafny, R. *see* Kahn, T.W.
Gantt, J.S. *see* Miller, S.S.
Gao, L. *see* Barker, S.J.
Gatehouse, A.M.R. *see* Rao, K.V.
Gatehouse, J.A. *see* Rao, K.V.
Geigenberger, P. *see* Trethewey, R.N.
Gerrits, N. *see* Rook, F.
Geurts, R. *see* Albrecht, C.
Giegé, P., Konthur, Z., Walter, G. and Brennicke, A. *An ordered* Arabidopsis thaliana *mitochondrial cDNA library on high-density filters allows rapid systematic analysis of plant gene expression: a pilot study* 721
Gilmore, J. *see* Ruan, Y.
Gingerich, D. *see* Faure, J.-D.
Girke, T., Schmidt, H., Zähringer, U., Reski, R. and Heinz, E. *Identification of a novel Δ6-acyl-group desaturase by targeted gene disruption in* Physcomitrella patens 39
Gleave, A.P. *see* Atkinson, R.G.
Glover, J., Grelon, M., Craig, S., Chaudhury, A. and Dennis, E. *Cloning and characterisation of* MS5 *from* Arabidopsis*: a gene critical in male meiosis* 345
Goekjian, V.H. *see* Cheong, Y.H.
Gorgé, J.L. *see* Jaramillo, J.L.
Graham, N.S. *see* Maathius, F.J.M.
Green, E.F. *see* Perfect, S.E.
Green, J.R. *see* Perfect, S.E.
Gregerson, R.G. *see* Miller, S.S.
Grelon, M. *see* Glover, J.
Grierson, D. *see* Hamilton, A.J.
Grohmann, L. *see* Zabaleta, E.
Gunning, B.E.S. *see* Blackman, L.M.
Guo, A., Durner, J. and Klessig, D.F. *Characterization of a tobacco epoxide hydrolase gene induced during the resistance response to TMV* 647

Hackert, A. *see* Hahn, D.
Hahn, D., Nickelsen, J., Hackert, A. and Kück, U. *Germination-related genes encoding proteolytic enzymes are expressed in the nucellus of developing wheat grains* 575
Hajirezaei, M.-R. *see* Trethewey, R.N.
Hakkert, J.C. *see* Van Der Meer, I.M.
Hamilton, A.J., Brown, S., Yuanhai, H., Ishizuka, M., Lowe, A., Solis, A.-G.A. and Grierson, D. *A transgene with repeated DNA causes high frequency, post-transcriptional suppression of ACC-oxidase gene expression in tomato* 737
Hawes, C. *see* Boevink, P.
Hayashizaki, Y. *see* Seki, M.
Hedrich, R. *see* Dietrich, P.
Heinlein, M. *see* Kahn, T.W.
Heinz, E. *see* Girke, T.
Heiser, V. *see* Zabaleta, E.
Hellyer, A. *see* Crombie, H.J.
Herrmann, P. *see* Luerßen, H.
Hill, S.A. *see* Sweetlove, L.J.
Hodges, T.K. *see* Rao, K.V.
Hong, J.C. *see* Cheong, Y.H.
Hong, S.H. *see* Kim, B.C.
Hooley, R. *see* Lovegrove, A.
Horng, J.-T. *see* Pool, M.R.
Howell, S.H. *see* Faure, J.-D.
Hudson, M. and Smith, H. *The phytochrome B encoded by the* HLG *locus of* Nicotiana plumbaginifolia *is required for detection of photoperiod:* hlg *mutants show altered regulation of flowering and circadian movement* 281

Inzé, D. *see* Babiychuk, E.
Ipacs, I. *see* Kovács, I.
Ishizuka, M. *see* Hamilton, A.J.
Isshiki, M., Morino, K., Nakajima, M., Okagaki, R.J., Wessler, S.R., Izawa, T. and Shimamoto, K. *A naturally occurring functional allele of the rice* waxy *locus has a GT to TT mutation at the 5′ splice site of the first intron* 133
Itoh, H. *see* Tanaka-Ueguchi, M.
Iuchi, S. *see* Mikami, K.
Izawa, T. *see* Isshiki, M.

Jamet, E. *see* Uchida, K.
Janssen, B.-J. *see* Atkinson, R.G.
Jaramillo, J.L., Chueca, A., Sahrawy, M. and Gorgé, J.L. *Hybrids from pea chloroplast thioredoxins* f *and* m*: physicochemical and kinetic characteristics* 155
Jelitto, T.C. *see* Maathius, F.J.M.

Kahn, T.W., Lapidot, M., Heinlein, M., Reichel, C., Cooper, B., Gafny, R. and Beachy, R.N. *Domains of the TMV movement protein involved in subcellular localization* 15
Katagiri, T. *see* Mikami, K.
Kato, A. *see* Yokoyama, R.
Kauffeldt, C. *see* Rutledge, R.
Kende, H. *see* Cho, H.-T.
Kerry, M. *see* Brown, I.
Key, J.L. *see* Cheong, Y.H.
Kim, B.C., Soh, M.S., Hong, S.H., Furuya, M. and Nam, H.G. *Photomorphogenic development of the* Arabidopsis shy2–1D *mutation and its interaction with phytochromes in darkness* 61
Kim, B.C., Tennessen, D.J. and Last, R.L. *UV-B-induced photomorphogenesis in* Arabidopsis thaliana 667
Kirik, V. *see* Luerßen, H.
Klee, H.J. *see* Lashbrook, C.C.
Klessig, D.F. *see* Guo, A.
Komeda, Y. *see* Yokoyama, R.
Konthur, Z. *see* Giegé, P.
Koops, A.J. *see* Van Der Meer, I.M.
Kortstee, A. *see* Rook, F.
Koshioka, M. *see* Tanaka-Ueguchi, M.
Kossmann, J. *see* Sweetlove, L.J.
Kovács, I., Ayaydin, F., Oberschall, A., Ipacs, I., Bottka, S., Pongor, S., Dudits, D. and Tóth, E.C. *Immunolocalization of a novel annexin-like protein encoded by a stress and abscisic acid responsive gene in alfalfa* 185
Kragler, F., Monzer, J., Shash, K., Xoconostle-Cázares, B. and Lucas, W.J. *Cell-to-cell transport of proteins: requirement for unfolding and characterization of binding to a putative plasmodesmal receptor* 367
Kück, U. *see* Hahn, D.
Kudia, J. *see* Xu, Q.
Kuo, J. *see* Zhang, W.H.
Kushnir, S. *see* Babiychuk, E.
Kutchan, T.M. *see* Chou, W.-M.

Lamppa, G.K. *see* Wan, J.
Lapeyrie, F. *see* Albrecht, C.
Lapidot, M. *see* Kahn, T.W.
Lashbrook, C.C., Tieman, D.M. and Klee, H.J. *Differential regulation of the tomato* ETR *gene family throughout plant development* 243
Last, R.L. *see* Kim, B.C.
Laudert, D. and Weiler, E.W. *Allene oxide synthase: a major control point in* Arabidopsis thaliana *octadecanoid signalling* 675
Lebrun-Garcia, A., Ouaked, F., Chiltz, A. and Pugin, A. *Activation of MAPK homologues by elicitors in tobacco cells* 773
Lehman, C.C. *see* Staswick, P.E.
Lemcke, K. and Schmülling, T. *Gain of function assays identify non-*rol *genes from* Agrobacterium rhizogenes *TL-DNA that alter plant morphogenesis or hormone sensitivity* 423
Liang, S. *see* Xu, Q.
Llaca, V. and Messing, J. *Amplicons of maize zein genes are conserved within genic but expanded and constricted in intergenic regions* 211
López-Huertas, E. *see* Pool, M.R.
Lovegrove, A., Barratt, D.H.P., Beale, M.H. and Hooley, R. *Gibberellin-photoaffinity labelling of two polypeptides in plant plasma membranes* 311
Lowe, A. *see* Hamilton, A.J.
Luan, S. *see* Xu, Q.
Lucas, W.J. *see* Kragler, F.
Luerßen, H., Kirik, V., Herrmann, P. and Miséra, S. FUSCA3 *encodes a protein with a conserved VP1/AB13-like B3 domain which is of functional importance for the regulation of seed maturation in* Arabidopsis thaliana 755
Lyon, J. *see* Simpson, C.G.

Maathius, F.J.M., May, S.T., Graham, N.S., Bowen, H.C., Jelitto, T.C., Trimmer, P., Bennett, M.J., Sanders, D. and White, P.J. *Cell marking in* Arabidopsis thaliana *and its application to patch-clamp studies* 843
Mansfield, J. *see* Brown, I.
Marc-Martin, S. *see* Di Sansebastiano, G.-P.
Martin, B. *see* Boevink, P.
Más, P. and Beachy, R.N. *Distribution of TMV movement protein in single living protoplasts immobilized in agarose* 835
Matsuoka, M. *see* Tanaka-Ueguchi, M.
May, S.T. *see* Maathius, F.J.M.
McConn, M., and Browse, J. *Molecular characterization of a plant FKBP12 that does not mediate action of FK506 and rapamycin* 521
McQuade, C. *see* Simpson, C.G.
Meinke, D.W. *see* Nickle, T.C.
Messing, J. *see* Llaca, V.
Meyer, P. *see* Van Blokland, R.
Mikami, K., Katagiri, T., Iuchi, S., Yamaguchi-Shinozaki, K. and Shinozaki, K. *Co- and/or post-translational modifications are critical for TCH4 XET activity* 563
Miller, S.S., Driscoll, B.T., Gregerson, R.G., Gantt, J.S. and Vance, C.P. *Alfalfa malate dehydrogenase (MDH): molecular cloning and characterization of five different forms reveals a unique nodule-enhanced MDH* 173
Miséra, S. *see* Luerßen, H.
Monzer, J. *see* Kragler, F.
Moons, A., Valcke, R. and Van Montagu, M. *Low-oxygen stress and water deficit induce cytosolic pyruvate orthophosphate dikinase (PPDK) expression in roots of rice, a $C_3$ plant* 89
Morino, K. *see* Isshiki, M.
Morris, B.A.M. *see* Atkinson, R.G.
Mueller-Klieser, W. *see* Borisjuk, L.
Muramatsu, T. *see* Uchida, K.

Nagao, R.T. *see* Cheong, Y.H.
Nakajima, M. *see* Isshiki, M.
Nam, H.G. *see* Kim, B.C.
Neuhaus, J.-M. *see* Di Sansebastiano, G.-P.
Nickelsen, J. *see* Hahn, D.
Nickle, T.C. and Meinke, D.W. *A cytokinesis-defective mutant of* Arabidopsis (cyt1) *characterized by embryonic lethality, incomplete cell walls, and excessive callose accumulation* 321
Nicolas, O. *see* Rutledge, R.
Nilsson, O., Wu, E., Wolfe, D.S. and Weigel, D. *Genetic ablation of flowers in transgenic* Arabidopsis 799
Nishiyama, Y. *see* Seki, M.
Nong, T. *see* Fennoy, S.L.
Northrop, F. *see* Zeeman, S.C.

O'Connell, R.J. *see* Perfect, S.E.
O'Connor, P.J. *see* Barker, S.J.
O'Farrell, M.K. *see* Babiychuk, E.
Oberschall, A. *see* Kovács, I.
Ohme-Takagi, M. *see* Suzuki, K.
Okagaki, R.J. *see* Isshiki, M.

Oparka, K. *see* Boevink, P.
Ouaked, F. *see* Lebrun-Garcia, A.
Overall, R.L. *see* Blackman, L.M.
Oyama, N. *see* Tanaka-Ueguchi, M.

Paris, N. *see* Di Sansebastiano, G.-P.
Park, J.M. *see* Cheong, Y.H.
Perfect, S.E., O'Connell, R.J., Green, E.F., Doering-Saad, C. and Green, J.R. *Expression cloning of a fungal proline-rich glycoprotein specific to the biotrophic interface formed in the* Colletotrichum*-bean interaction* 273
Phillips, J. *see* Frank, W.
Pongor, S. *see* Kovács, I.
Pool, M.R, López-Huertas, E., Horng, J.-T. and Baker, A. *NADPH is a specific inhibitor of protein import into glyoxysomes* 1
Powell, K.S. *see* Rao, K.V.
Prat, S. *see* Carrera, E.
Puente, P. *see* Chattopadhyay, S.
Pugin, A. *see* Lebrun-Garcia, A.

Qi, Q. *see* Wang, H.

Rao, K.V., Rathore, K.S., Hodges, T.K., Fu, X., Stoger, E., Sudhakar, D., Williams, S., Christou, P., Bharathi, M., Bown, D.P, Powell, K.S., Spence, J., Gatehouse, A.M.R. and Gatehouse, J.A. *Expression of snowdrop lectin (GNA) in transgenic rice plants confers reistance to rice brown planthopper* 469
Rathore, K.S. *see* Rao, K.V.
Regan, S. *see* Rutledge, R.
Reichel, C. *see* Kahn, T.W.
Reid, J.S.G. *see* Crombie, H.J.
Rengel, Z. *see* Zhang, W.H.
Reski, R. *see* Girke, T.
Rhee, S.Y. and Somerville, C.R. *Tetrad pollen formation in quartet mutants of* Arabidopsis thaliana *is associated with persistence of pectic polysaccharides of the pollen mother cell wall* 79
Riedel, K. *see* Trethewey, R.N.
Riesmeier, J.W. *see* Sweetlove, L.J.
Riesmeier, J.W. *see* Trethewey, R.N.
Rook, F., Gerrits, N., Kortstee, A., Van Kampen, M., Borrias, M., Weisbeek, P. and Smeekens, S. *Sucrose-specific signalling represses translation of the* Arabidopsis ATB2 *bZIP transcription factor gene* 253
Ross, S. *see* Van Blokland, R.
Rouster, J., Van Mechelen, J. and Cameron-Mills, V. *The untranslated leader sequence of the barley* lipoxygenase 1 (Lox1) *gene confers embryo-specific expression* 435
Ruan, Y., Gilmore, J. and Conner, T. *Towards* Arabidopsis *genome analysis: monitoring expression profiles of 1400 genes using cDNA microarrays* 821
Runeberg-Roos, P. and Saarma, M. *Phytepsin, a barley vacuolar aspartic proteinase, is highly expressed during autolysis of developing tracheary elements and sieve cells* 139
Rutledge, R., Regan, S., Nicolas, O., Fobert, P., Côté, C., Bosnich, W., Kauffeldt, C., Sunohara, G., Séguin, A. and Stewart, D. *Characterization of an* AGAMOUS *homologue from the conifer black spruce (*Picea mariana*) that produces floral homeotic conversions when expressed in* Arabidopsis 625
Ryu, G.R. *see* Cheong, Y.H.

Saarma, M. *see* Runeberg-Roos, P.
Sahrawy, M. *see* Jaramillo, J.L.
Salamini, F. *see* Frank, W.
Sanders, D. *see* Maathius, F.J.M.
Santa Cruz, S. *see* Boevink, P.
Schmidt, H. *see* Girke, T.
Schmülling, T. *see* Lemcke, K.
Schopfer, P. *see* Fischer, K.
Schorr, P. *see* Wang, H.
Scollan, C. *see* Van Blokland, R.
Séguin, A. *see* Rutledge, R.
Seki, M., Carninci, P., Nishiyama, Y., Hayashizaki, Y. and Shinozaki, K. *High-efficiency cloning of* Arabidopsis *full-length cDNA by biotinylated CAP trapper* 707
Shash, K. *see* Kragler, F.
Shimamoto, K. *see* Isshiki, M.
Shinozaki, K. *see* Mikami, K.
Shinozaki, K. *see* Seki, M.
Shinshi, H. *see* Suzuki, K.
Simpson, C.G., McQuade, C., Lyon, J. and Brown, J.W.S. *Characterization of exon skipping mutants of the* COP1 *gene from* Arabidopsis 125
Singh, D.P. *see* Chow, K.S.
Slabaugh, M. *see* Dehesh, K.
Smeekens, S. *see* Rook, F.
Smith, A.G. *see* Chow, K.S.
Smith, A.M. *see* Zeeman, S.C.
Smith, C.P. *see* West, C.E.
Smith, H. *see* Hudson, M.
Smith, S.E. *see* Barker, S.J.
Soh, M.S. *see* Kim, B.C.
Solis, A.-G.A. *see* Hamilton, A.J.
Somerville, C.R. *see* Rhee, S.Y.
Sonnewald, U. *see* Trethewey, R.N.
Spence, J. *see* Rao, K.V.
Staswick, P.E., Yuen, G.Y. and Lehman, C.C. *Jasmonate signaling mutants of* Arabidopsis *are susceptible to the soil fungus* Pythium irregulare 747
Stephens, S.M. *see* West, C.E.
Stewart, D. *see* Rutledge, R.
Stitt, M. *see* Trethewey, R.N.
Stoger, E. *see* Rao, K.V.
Storozhenko, S. *see* Babiychuk, E.
Stummer, B. *see* Barker, S.J.
Sudhakar, D. *see* Rao, K.V.
Sunohara, G. *see* Rutledge, R.
Suzuki, K., Suzuki, N., Ohme-Takagi, M. and Shinshi, H. *Immediate early induction of mRNAs for ethylene-responsive transcription factors in tobacco leaf strips after cutting* 657
Suzuki, N. *see* Suzuki, K.
Svenson, M. *see* Tandre, K.
Svensson, M.E. *see* Tandre, K.
Sweetlove, L.J., Kossmann, J., Riesmeier, J.W., Trethewey, R.N. and Hill, S.A. *The control of source to sink carbon flux during tuber development in potato* 697

Takahashi, T. *see* Yokoyama, R.
Tanaka-Ueguchi, M., Itoh, H., Oyama, N., Koshioka, M. and Matsuoka, M. *Over-expression of a tobacco homeobox gene,* NTH15, *decreases the expression of a gibberellin biosynthetic gene encoding GA 20-oxidase* 391
Tandre, K., Svenson, M., Svensson, M.E. and Engström, P. *Conservation of gene structure and activity in the regulation of reproductive organ development of conifers and angiosperms* 615
Tennessen, D.J. *see* Kim, B.C.

Tieman, D.M. *see* Lashbrook, C.C.
Torii, K.U. *see* Yokoyama, R.
Tóth, E.C. *see* Kovács, I.
Trethewey, R.N. *see* Sweetlove, L.J.
Trethewey, R.N., Geigenberger, P., Riedel, K., Hajirezaei, M.-R., Sonnewald, U., Stitt, M., Riesmeier, J.W. and Willmitzer, L. *Combined expression of glucokinase and invertase in potato tubers leads to a dramatic reduction in starch accumulation and stimulation of glycolysis* 109
Trethowan, J. *see* Brown, I.
Trimmer, P. *see* Maathius, F.J.M.

Uchida, K., Muramatsu, T., Jamet, E. and Furuya, M. *Control of expression of a gene encoding an extensin by phytochrome and a blue light receptor in spores of* Adiantum capillus-veneris L 813

Valcke, R. *see* Moons, A.
Van Blokland, R., Ross, S., Corrado, G., Scollan, C. and Meyer, P. *Two different genes encode ferrochelatase in Arabidopsis: mapping, expression and subcellular targeting of the precursor proteins* 543
Van Der Meer, I.M., Koops, A.J., Hakkert, J.C. and Van Tunen, A.J. *Anions permeate and gate GCAC1, a voltage-dependent guard cell anion channel* 489
Van Kampen, M. *see* Rook, F.
Van Mechelen, J. *see* Rouster, J.
Van Montagu, M. *see* Babiychuk, E.
Van Montagu, M. *see* Moons, A.
Van Tunen, A.J. *see* Van Der Meer, I.M.
Vance, C.P. *see* Miller, S.S.

Walenta, S. *see* Borisjuk, L.
Walker, A.R. *see* Chow, K.S.
Walter, G. *see* Giegé, P.
Wan, J., Bringloe, D. and Lamppa, G.K. *Disruption of chloroplast biogenesis and plant development upon down-regulation of a chloroplast processing enzyme involved in the import pathway* 459
Wang, H., Qi, Q., Schorr, P., Cutler, A.J., Crosby, W.L. and Fowke, L.C. *Cloning of the fructan biosynthesis pathway of Jerusalem artichoke* 501
Waterworth, W.M. *see* West, C.E.
Weber, H. *see* Borisjuk, L.
Wei, N. *see* Chattopadhyay, S.
Weigel, D. *see* Nilsson, O.
Weiler, E.W. *see* Laudert, D.
Weisbeek, P. *see* Rook, F.
Wessler, S.R. *see* Isshiki, M.
West, C.E., Waterworth, W.M., Stephens, S.M., Smith, C.P. and Bray, C.M. *Cloning and functional characterisation of a peptide transporter expressed in the scutellum of barley grain during the early stages of germination* 221
White, P.J. *see* Maathius, F.J.M.
Williams, S. *see* Rao, K.V.
Willmitzer, L. *see* Trethewey, R.N.
Willows, R.D. *see* Cornejo, J.
Wobus, U. *see* Borisjuk, L.
Wolfe, D.S. *see* Nilsson, O.
Wu, E. *see* Nilsson, O.

Xoconostle-Cázares, B. *see* Kragler, F.
Xu, Q., Liang, S., Kudia, J. and Luan, S. *ICK1, a cyclin-dependent protein kinase inhibitor from* Arabidopsis thaliana *interacts with both Cdc2a and CycD3, and its expression is induced by abscisic acid* 511

Yamaguchi-Shinozaki, K. *see* Mikami, K.
Yang, C.-H. *see* Chou, M.-L.
Yokoyama, R., Takahashi, T., Kato, A., Torii, K.U. and Komeda, Y. *The Arabidopsis* ERECTA *gene is expressed in the shoot apical meristem and organ primordia* 301
Yoo, C.M. *see* Cheong, Y.H.
Yu, S.-M. *see* Chan, M.-T.
Yuanhai, H. *see* Hamilton, A.J.
Yuen, G.Y. *see* Staswick, P.E.

Zabaleta, E., Heiser, V., Grohmann, L. and Brennicke, A. *Promoters of nuclear-encoded respiratory chain Complex I genes from* Arabidopsis thaliana *contain a region essential for anther/pollen-specific expression* 49
Zähringer, U. *see* Girke, T.
Zeeman, S.C., Northrop, F., Smith, A.M. and Ap Rees, T. *A starch-accumulating mutant of* Arabidopsis thaliana *deficient in a chloroplastic starch-hydrolysing enzyme* 357
Zhang, W.H., Rengel, Z. and Kuo, J. *Determination of intracellular* $Ca^{2+}$ *in cells of intact wheat roots: loading of acetoxymethyl ester of Fluo-3 under low temperature* 147
Zubko, M.K. and Day, A. *Stable albinism induced without mutagenesis: a model for ribosome-free plastid inheritance* 265

*The Plant Journal* (1998) **15**(6), 859–862

# Subject index

AB13 755
ABA 89
abscisic acid 413, 501, 563, 765
abscission 243
ACC-oxidase 737
actin 441
*AGAMOUS*-like 625
agarose-embedment 835
*Agrobacterium rhizogenes* 423
aleurone 311
alfalfa 173
allene oxide cyclase 675
allene oxide synthase 675
amylase 357
α-amylase gene 685
anion channel 479
anion permeation 479
anion-dependent gating 479
annexin 185
anomalous mole fraction 479
anther 49
antibody 185
antisense gene 459
apicalmeristem 301
APP 635
*Arabidopsis* 69, 253, 265, 301, 311, 321, 345, 357, 553, 747, 821
*Arabidopsis* mutant 125
*Arabidopsis thaliana* 49, 61, 501, 563, 635, 707, 721, 843
arachidonic acid 39
aspartic proteinase 139
autolysis 139
autotrophy 521
auxin 423

B3 domain 755
baculovirus 553
barley 435
benzophenanthridine 289
benzylisoquinoline 289
β-glucosidase 27
biliverdin 99
biotinylated CAP trapper 707
biotrophy 273
blue light receptor 813
*Brassica* 265
bZIP motif 199
bZIP transcription factor 253

calcineurin 511
callose synthase 333
callose 79, 321
carbohydrate state 583
carbon partitioning 697
carboxypeptidase 569
CBPRP 333
Cdc2a 501
CDK inhibitor ICK1 501
cDNA 185
cDNA library 707
cell ablation 799
cell expansion 805
cell wall 165, 333, 553
cell wall (plant) 27
cell wall loosening 805
cell walls 321
cell-to-cell communication 401
cell-to-cell movement 367
chalcone synthase 593
*Chara* 401
*Chlamydomonas reinhardtii* 575
chloroplast 155
chloroplast processing enzyme 459
chloroplast psaA gene 575
chloroplasts 357
chromosome mapping 531
cold loading 147
coleoptile 119
*Colletotrichum* 273
comparative genetics 211
cone 625
confocal microscopy 791, 835
conifer 625
COP/DET/FUS 667
co-suppression 737
*Craterostigma plantagineum* 413
cryptochrome 667
cryptogein 773
C-terminal propeptide 449
*Cuphea* 383
cyanobacteria 99
CycD3 (cyclin δ3) 501
cycloheximide 657
cytochrome P-450 289
cytokinesis 321
cytokinin 423
cytoplasmic calcium 147
cytosolic PPDK 89

$^{6m}$dA methylation 543
*DAL2* 615
*dam* enzyme 543
dark phenotype 61
deepwater rice 805
desaturase 521
6-desaturase 39
development 459, 625
developmental phase transitions 231
dichlobenil 321
differential display 813
diphtheria toxin 799
disease resistance 747
DNA binding proteins 413
DNA repair 635
DNA-binding protein 199
domain mapping 501
double mutant analysis 231
drought 765

embryo 435
embryo-defective mutants 321
embryogenesis 755
3′ end processing 575

© 1998 Blackwell Science Ltd

endomycorrhiza 605
endosperm 569
endotransglycosylation 553
*ENOD* 605
enzyme activation 155
episome 593
ERD2 441
*ERECTA* 301
ethylene 243, 657, 675
ethylene-responsive element 657
ethylene-responsive transcription factors 657
*ETR* 243
exine 79
exon 125
exon definition 125
expansin 805
expression in yeast 39
extensin 813

FAD 289
fatty acid 521
fatty acid biosynthesis 383
fern spore 813
ferrochelatase 531
1-*fft* 489
FKBP 511
*FLD* 231
floral induction 799
floral transition 231
flower development 799
fluence rate 667
Fluo-3 147
fluorescence microscopy 15
French bean 333
fructan biosynthesis 489
fructan genes 489
fructose-1,6-bisphosphatase 155
fruit ripening 243
full-length cDNA 707
functional genomics 821
FUS3 755

GA biosynthesis 391
GA 20-oxidase 391
geminivirus 593
gene conversion 211
gene disruption 39
gene expression 531, 563, 813, 821
gene families 173
gene phylogeny 615
gene silencing 593, 737
genome analysis 821
genome stability 211
germin 165
germination 221, 243
GFP 15, 441, 835
gibberellin 311, 391
γ-linolenic acid 39
glucokinase 109
glucose gradients 583
glycolysis 109
glyoxysomes 1
grain development 569
gravitropism 119
green fluorescent protein (GFP) 449, 843
guard cell 479
GUS assays 49

haem biosynthesis 531
HD-Zip genes 413
heme oxygenase 99
hemicellulose 27
heterodimerization 199
high-density filters 721
homeobox gene 391
homeotic 625
*Hordeum vulgare* 221
*hy* 667
hybrids 155
hydrogen peroxide 165

immunogold localisation 333
immunolocalization 185, 469
import 459
*in situ* hybridization 805
*in vivo* DNA methylation 543
inflorescence 301
inheritance 265
insect resistance 469
intron 125, 615
invertase 109

jasmonate 765
jasmonic acid 675, 747
Jerusalem artichoke 489

*Kas4* 383
3-ketoacyl-ACP synthase IV 383

late-flowering 231
leader sequence 435
leaf morphology 391
leaf starch 357
*LEAFY* 799
light regulation 69
light signal transduction 61
lipoxygenase 435
low-oxygen stress 89
*Lox1* 435
*Lycopersicon esculentum* 791

MADS box 615, 625
maize 727
malate dehydrogenase 173
male-sterile mutant 345
MAPK 773
mechanosensor 119
*Medicago sativa* 185
medium-chain 383
meiosis 345
membrane-patch voltage clamp (patch-clamp) 843
metabolic control analysis 697
microarray 821
microsporogenesis 79
microtubules 119
mitochondria 49
mitochondrial cDNA library 721
mitotic activity 583
molecular cloning 563

monoterpenoid indole alkaloid 289
movement protein 835
mRNA splicing 133
mRNA stability 685
multigene family 211
mutant 69, 747
mutation 133

NADPH 1
NADP-malate dehydrogenase 155
nasturtium 27
nitrogen assimilation 173
Nod factors 605
nodule 173, 605
Norway spruce 615
*NTH15* 391
nucellus 569

octadecanoid biosynthesis 675
organelle targeting 531
organogenesis 805
ovuliferous scale 615
oxalate oxidase 165
oxidative damage 647
oxidoreductase 289
2-oxoglutarate 289
12-oxophytodienoic acid 675
oxygen-deprivation 727

papilla formation 333
pea 155
pectin 79
peptide transport 221
peroxidase 333
peroxisomes 1
petunia 593
*Phaseolus vulgaris* 333
phloem 469
phosphatidylinositol-4-phosphate 5-Kinase 563
photoaffinity 311
photomorphogenesis 61
photoreceptor 69
phototropism 119
phycobilins 99
*Physcomitrella* 39
phytepsin 139
phytochrome 61, 667, 813
phytochromobilin 99
pigments 99
plant 667
plant disease resistance 647
plant gene expression 721
plant genomics 211
plant Golgi 441
plant morphogenesis 423
plasma membrane 311
plasmodesmal receptor 367
plasmodesmal size exclusion limit 367
plasmodesmata 15, 401
plasmodesmata-associated protein 401
plastids 265
poly(ADP-ribose) polymerase 635
pore size 479
post-transcriptional 737
post-transcriptional regulation 727
potassium ($K^+$) channel 843
potato 109
potato (*Solanum tuberosum*) 697
pre-mRNA splicing 125
primexine 79
proline-rich protein 273
promoter 69, 435
promoter structure 49
protein import 1
protein isolation 401
protein kinase 773
protein targeting 15
protein translocation and unfolding 367
protoplasts 449
*Pythium irregulare* 747

real-time analysis 835
receptor 243
recessive mutant 791
redox regulation 511
repeat 737
resource allocation 697
respiratory chain complex I 49
ribosomes 265
rice 89, 133, 685
rice (*Oryza sativa*) 469
root 727, 843
root apical cells 147
roots 89

salicylic acid 647, 675
scutellum 221
seed development 583
seed 27
seed oil 383
senescence 243
*sex* mutant 357
shoot development 231
shotgun sequencing 211
SHY2 61
sialyl transferase 441
sieve cell 139
signal perception 243
signal transduction 311, 511, 667
signaling 747
sink 697
snowdrop lectin (GNA) 469
source 697
soybean 199
spectinomycin 265
5′ splice site 133
splice site selection 125
splicing 755
1-*sst* 489
starch 109
starch accumulation 583
starch degradation 357
stress response 185
sucrose 253
sugar repression 685
*sym8* 605

T-DNA 345, 423
tetrad pollen 79
TGACG-motif 199
thioesterase 383
thiol-protease 569
thioredoxin 155
tissue specific gene expression 49
tobacco 657, 773
tracheary element 139
transcript profiling 821
transcription factor 199
transcription regulation 69
transduction 773
transgenic Petunia 489
transgenic plants 15, 383, 423, 469, 543, 799
transglycosylase 27
transient assay 685
translational regulation 253
*trans*-splicing 575
*Tropaeolum* 27
tubers 109

unsaturation 521
3′ untranslated region 685
UV 667

VA mycorrhiza 791
vacuolar biogenesis 139
vacuolar pH 449
vacuolar targeting 449
vacuole types 449
*Vicia faba* 583
virus movement 15
virus protein distribution 835
VP1 755

water deficit 89
water stress 413, 563
*waxy* gene 133
wheat 569
wheat (*Triticum aestivum* L.) 147
wheat embryo 165
wounding 657, 675
wound-signalling 765

XTR 553
xyloglucan 27, 553

yeast two-hybrid system 413

*Zea* 119
*Zea mays* 727
zinc finger protein 199
Zn-finger-containing polymerase 635